

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/846,658A

1642

Page # 9

DATE: 06/09/98

TIME: 08:43:23

INPUT SET: S26559.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Adair, John R.
6 Athwal, Diljeet S.
7 Emtage, John S.
8
9 (ii) TITLE OF INVENTION: Humanised Antibodies
10
11 (iii) NUMBER OF SEQUENCES: 30
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
15 (B) STREET: One Liberty Place - 46th Floor
16 (C) CITY: Philadelphia
17 (D) STATE: PA
18 (E) COUNTRY: USA
19 (F) ZIP: 19103
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: US 08/846,658
29 (B) FILING DATE: 01-MAY-1997
30 (C) CLASSIFICATION:
31
32 (viii) ATTORNEY/AGENT INFORMATION:
33 (A) NAME: Trujillo, Doreen Yatko
34 (B) REGISTRATION NUMBER: 35,719
35 (C) REFERENCE/DOCKET NUMBER: CARP-0057
36
37 (ix) TELECOMMUNICATION INFORMATION:
38 (A) TELEPHONE: (215) 568-3100
39 (B) TELEFAX: (215) 568-3439
40
41
42 (2) INFORMATION FOR SEQ ID NO:1:
43
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 20 base pairs
46 (B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear
49

50 (ii) MOLECULE TYPE: cDNA
51
52

53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
54

55 TCCAGATGTT AACTGCTCAC
56

20

57 (2) INFORMATION FOR SEQ ID NO:2:
58

59 (i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 23 base pairs
61 (B) TYPE: nucleic acid
62 (C) STRANDEDNESS: single
63 (D) TOPOLOGY: linear
64

65 (ii) MOLECULE TYPE: cDNA
66
67
68

69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
70

71 CAGGGGCCAG TGGATGGATA GAC
72

23

73 (2) INFORMATION FOR SEQ ID NO:3:
74

75 (i) SEQUENCE CHARACTERISTICS:
76 (A) LENGTH: 9 amino acids
77 (B) TYPE: amino acid
78 (C) STRANDEDNESS: single
79 (D) TOPOLOGY: linear
80

81 (ii) MOLECULE TYPE: peptide
82
83
84

85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
86

87 Leu Glu Ile Asn Arg Thr Val Ala Ala
88 1 5
89

90 (2) INFORMATION FOR SEQ ID NO:4:
91

92 (i) SEQUENCE CHARACTERISTICS:
93 (A) LENGTH: 943 base pairs
94 (B) TYPE: nucleic acid
95 (C) STRANDEDNESS: single
96 (D) TOPOLOGY: linear
97

98 (ii) MOLECULE TYPE: cDNA
99

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100
101 (ix) FEATURE:
102 (A) NAME/KEY: CDS
103 (B) LOCATION: 18..722
104
105 (ix) FEATURE:
106 (A) NAME/KEY: mat_peptide
107 (B) LOCATION: 84..722
108
109
110 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
111
112 GAATTCCCAA AGACAAA ATG GAT TTT CAA GTG CAG ATT TTC AGC TTC CTG 50
113 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu
114 -22 -20 -15
115
116 CTA ATC AGT GCC TCA GTC ATA ATA TCC AGA GGA CAA ATT GTT CTC ACC 98
117 Leu Ile Ser Ala Ser Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr
118 -10 -5 1 5
119
120 CAG TCT CCA GCA ATC ATG TCT GCA TCT CCA GGG GAG AAG GTC ACC ATG 146
121 Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met
122 10 15 20
123
124 ACC TGC AGT GCC AGC TCA AGT GTA AGT TAC ATG AAC TGG TAC CAG CAG 194
125 Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln
126 25 30 35
127
128 AAG TCA GGC ACC TCC CCC AAA AGA TGG ATT TAT GAC ACA TCC AAA CTG 242
129 Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu
130 40 45 50
131
132 GCT TCT GGA GTC CCT GCT CAC TTC AGG GGC AGT GGG TCT GGG ACC TCT 290
133 Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser
134 55 60 65
135
136 TAC TCT CTC ACA ATC AGC GGC ATG GAG GCT GAA GAT GCT GCC ACT TAT 338
137 Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr
138 70 75 80 85
139
140 TAC TGC CAG CAG TGG AGT AGT AAC CCA TTC ACG TTC GGC TCG GGG ACA 386
141 Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr
142 90 95 100
143
144 AAG TTG GAA ATA AAC CGG GCT GAT ACT GCA CCA ACT GTA TCC ATC TTC 434
145 Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Val Ser Ile Phe
146 105 110 115
147
148 CCA CCA TCC AGT GAG CAG TTA ACA TCT GGA GGT GCC TCA GTC GTG TGC 482
149 Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys
150 120 125 130
151
152 TTC TTG AAC AAC TTC TAC CCC AAA GAC ATC AAT GTC AAG TGG AAG ATT 530

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153 Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile
154      135                      140                      145
155
156
157 GAT GGC AGT GAA CGA CAA AAT GGC GTC CTG AAC AGT TGG ACT GAT CAG      578
158 Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln
159 150                      155                      160                      165
160
161 GAC AGC AAA GAC AGC ACC TAC AGC ATG AGC AGC ACC CTC ACG TTG ACC      626
162 Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr
163                      170                      175                      180
164
165 AAG GAC GAG TAT GAA CGA CAT AAC AGC TAT ACC TGT GAG GCC ACT CAC      674
166 Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His
167                      185                      190                      195
168
169 AAG ACA TCA ACT TCA CCC ATT GTC AAG AGC TTC AAC AGG AAT GAG TGT      722
170 Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
171      200                      205                      210
172
173 TAGAGACAAA GGTCTTGAGA CGCCACCACC AGCTCCCAGC TCCATCCTAT CTTCCCTTCT      782
174
175 AAGGTCTTGG AGGCTTCCCC ACAAGCGCTT ACCACTGTTG CGGTGCTCTA AACCTCCTCC      842
176
177 CACCTCCTTC TCCTCCTCCT CCCTTTCCTT GGCTTTTATC ATGCTAATAT TTGCAGAAAA      902
178
179 TATTCAATAA AGTGAGTCTT TGCCTTGAAA AAAAAAAAAA A      943
180
181
182 (2) INFORMATION FOR SEQ ID NO:5:
183
184 (i) SEQUENCE CHARACTERISTICS:
185 (A) LENGTH: 235 amino acids
186 (B) TYPE: amino acid
187 (D) TOPOLOGY: linear
188
189 (ii) MOLECULE TYPE: protein
190
191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
192
193 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
194 -22      -20                      -15                      -10
195
196 Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
197      -5                      1                      5                      10
198
199 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
200                      15                      20                      25
201
202 Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser
203      30                      35                      40
204
205 Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro

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206          45          50          55
207
208 Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
209      60          65          70
210
211 Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
212      75          80          85          90
213
214
215 Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn
216          95          100          105
217
218 Arg Ala Asp Thr Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
219          110          115          120
220
221 Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
222          125          130          135
223
224 Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
225          140          145          150
226
227 Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
228          155          160          165          170
229
230 Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
231          175          180          185
232
233 Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
234          190          195          200
235
236 Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
237          205          210
238
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239 (2) INFORMATION FOR SEQ ID NO:6:

240

241 (i) SEQUENCE CHARACTERISTICS:

242 (A) LENGTH: 1570 base pairs

243 (B) TYPE: nucleic acid

244 (C) STRANDEDNESS: single

245 (D) TOPOLOGY: linear

246

247 (ii) MOLECULE TYPE: cDNA

248

249

250 (ix) FEATURE:

251 (A) NAME/KEY: CDS

252 (B) LOCATION: 41..1444

253

254 (ix) FEATURE:

255 (A) NAME/KEY: mat_peptide

256 (B) LOCATION: 98..1444

257

258

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SEQUENCE VERIFICATION REPORT
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Original Text